REMARKS

INTRODUCTION:

In accordance with the foregoing, claims 13-15 have been amended, and claims 24-26 have been added. No new matter is being presented, and approval and entry are respectfully requested.

Claims 13-15 and 24-26 are pending and under consideration. Reconsideration is respectfully requested.

REMOVAL OF CLAIM 22:

The Examiner pointed out that claim 22 should be removed since it had been cancelled. Claim 22 has been removed. Applicants thank the Examiner for pointing out the error.

SPECIFICATION:

The Examiner objected to the specification as failing to provide proper antecedent basis for the claimed subject matter. Specifically, the Examiner stated: "The specification does not disclose limitations regarding use of restriction condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set," and sets forth the argument that the statement "…it is determined …whether these attributes coincide" merely describes checking whether attributes coincide, but it does not teach limitation that the attributes do, in fact, coincide." Applicants respectfully disagree and explain their position as follows.

As stated on page 7, lines 10-19 of the specification:

An object of the invention is to provide method and apparatus capable of **automatically extracting and evaluating mutually coinciding or similar portions between sequences of atoms or atomic groups** in molecules such as protein molecules in accordance with a simple processing mechanism. (emphasis added)

Another object of the invention is to provide method and apparatus capable of **automatically extracting and evaluating mutually coinciding or similar portions between three-dimensional structures of the molecules** such as protein molecules. (emphasis added)

It is respectfully submitted that upon "determining whether attributes coincide," if the attributes do, in fact, coincide, one skilled in the art notes that such attributes are homologous, wherein homologous means having the same relative position, value, or structure. As noted on page 37, lines 1-10, of the specification:

The number of candidates for a point to be related can be reduced by **using an attribute**

of the point in relating an element a_i of a point set A to an element b_j of a point set B. The **attributes** of the point, for example, **include the type of an atom, an atomic group, and a molecule, the hydrophilic property, the hydrophobic property, and the positive or negative charge**. It is determined whether the point is selected as a candidate by **checking whether these attributes coincide.** (emphasis added)

Thus, in the present invention, an attribute is selected (such as the type of an atom, an atomic group, and a molecule, the hydrophilic property, the hydrophobic property, and the positive or negative charge), and if the attribute of a first point set is the same as the attribute of a second point set, the attributes are said to coincide. That is, for example, if the type of atom of a first point set is the same as the type of atom of the second point set, the attributes of the two point sets are said to coincide. For example, as stated on page 59, lines 17-20: "The correspondence is fixed only when the type of the two subsets are the same and when the r.m.s.d. value is smaller than the threshold value when the structures are best matched."

Page 26, line 17-page 27, line 34, of the specification further explains how sequences are matched so that portions that coincide are aligned:

> FIG. 10 shows an example of this display. The display example displays a processing result of two amino acid sequences: human cytochrome c and bacteria cytochrome c. The longest common subsequences are displayed in accordance with a display mode indicative of the interval at which they are arranged in the two amino acid sequences. More specifically, by adopting a mode of displaying "GD {x 3, 3} G {x 0, 1} K {x 0, 2} . . . ", the longest common subsequences are displayed as follows. In the human cytochrome c, "GD" is followed by **three characters that do not coincide**, followed by "G", which is immediately followed by "K". On the other hand, in the bacteria cytochrome c, "GD" is followed by **three characters that do not coincide**, followed by "G", which is **followed by one character that does not coincide**. "K" follows immediately thereafter. (emphasis added)

> The motif search unit 33 first **searches** the motif data base 60 **for the motif sequence being homologous with the input amino acid sequence based on the decision result of the homology decision unit** 31, and then **decides whether the homologous motif sequence is a true motif sequence** included in the input amino acid sequence **in accordance with the longest common subsequences determined by the LCS detection unit** 30 **and the length of the character sequence between the longest common subsequences.** (emphasis added)

> **Upon receipt of the longest common subsequences and their occurrence positions** that the LCS detection unit 30 detects, **the alignment unit 34 aligns the input amino acid sequence and the amino acid sequence given from the amino acid sequence data base 50 and the motif data base 60 so as to relate the longest common subsequence in one amino acid sequence to that in the other,** and displays the aligned amino acid sequences in the display device 42 through the display control unit 35. FIG. 12 shows an example of this display, which displays a processing result of two amino acid sequences: human cytochrome c and bacteria cytochrome c. The alignment processing is carried out by inserting a blank corresponding to the length of the character sequence between the positions of the subsequences. (emphasis added)

5

Hence, it is respectfully submitted that it is clear to one skilled in the art that there is a restriction condition that is utilized wherein attributes of two point sets are compared. The specification states that **first, the attributes of two point sets are compared to determine if they coincide** and **then specifies that if the attributes are the same, further comparison is utilized to determine if the two point sets coincide or are similar.** Clearly, such a comparison is made to allow evaluation of mutually coinciding or similar portions in sequences or molecules. For example, correspondence is fixed when the attributes are the same and when the r.m.s.d. value is less than a threshold value.

Thus, it is respectfully submitted that claim 13 is clear and is supported by the specification, and that the language of the specification supports the language of claim 13 that recites: "the restriction condition includes a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for combination of correspondence." Hence, it is respectfully submitted that the specification provides proper antecedent basis for the claimed subject matter.

REJECTION UNDER 35 U.S.C. §101:

A. In the Office Action, at pages 3-4, numbered paragraph 4, claims 13-15 were rejected under 35 U.S.C. §101 because the Examiner submitted that the claimed invention is directed to non-statutory subject matter. This rejection is traversed and reconsideration is requested.

B. In the Office Action, at pages 5-6, numbered paragraph 5, claims 13-15 were rejected under 35 U.S.C. §101 because the Examiner submitted that the claimed invention lacks patentable utility. This rejection is traversed and reconsideration is requested.

With respect to A and B above, it is respectfully submitted that the courts have held: "[T]he mere fact that a claimed invention involves inputting numbers, calculating numbers, outputting numbers, and storing numbers, in and of itself, would not render it nonstatutory subject matter ..." See State Street Bank & Trust Co. v. Signature Financial Group, 47 USPQ2d 1596, 1602 (Fed. Cir. 1998). To be patentable, an algorithm must be applied in a "useful" way. See State Street at 1601.

In In re Alappat, 31 USPQ2d 1545 (Fed. Cir. 1994), the Court held that "data, transformed by a machine through a series of mathematical calculations to produce a smooth waveform display on a rasterizer monitor, constituted a practical application of an abstract idea ... because it produced 'a useful, concrete and tangible result'–the smooth waveform." See State Street at 1601.

In addition, in <u>State Street</u>, the Court held that "the transformation of data, representing discrete dollar amounts, by a machine through a series of mathematical calculations into a final share price, constitutes a practical application of a mathematical algorithm, formula, or calculation, because it produces 'a useful, concrete and tangible result'–a final share price momentarily fixed for recording and reporting purposes..." See <u>State Street</u> at 1601.

The present invention relates to a method for extracting and evaluating mutually similar portions in one-dimensional sequences in molecules and/or three-dimensional structures of molecules, while facilitating the extraction and evaluation by **using a computer comparison of known and unidentified molecules**. Independent claim 13 has been amended to recite that method is implemented using a computer processor. Also, new claim 24 recites that a computer performs the method and that the correspondence/similarity determination is stored on a computer readable recording medium. Hence, it is respectfully submitted that **the claimed invention is directed to statutory subject matter**.

With respect to the Examiner's comments that the two point sets are not limited to any particular physical object, it is respectfully submitted that on page 28, lines 5-15, and lines 20 of page 28 through page 1 of page 29 the specification recites:

> For instance, it is assumed that there are substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ as shown in FIG. 13A and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ as shown in FIG. 13B. The elements constituting these substances A and B are related to each other as shown in FIG. 13C, and the substance B is rotated and moved so that the r.m.s.d value between the corresponding elements is minimized, as shown in FIG. 13D. The r.m.s.d value is obtained in the following equation wherein U denotes a rotation matrix and w_k denote respective weights: ...

> A technique of obtaining the rotation and movement of the substances which minimizes the r.m.s.d value between these corresponding points is proposed by Kabsh et al. as described above, and is presently widely used.

> 1. Various Methods of Determining Correspondence

> (1) Generation of Correspondence of Point Sets that are Not Ordered

> The substances A and B are expressed, respectively, by the point sets $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$, $1 \leq i \leq m$, and the point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$, $1 \leq j \leq n$. The respective points $a_i =(x_i, y_i, z_i)$ and $b_j =(x_j, y_j, z_j)$ are expressed as a three-dimensional coordinate. In this case, the correspondence of elements between these point sets is in principle obtained by relating sequentially the points in the respective sets, and it can be accomplished to generate all combinations by creating a tree construction as shown in FIG. 14A.

Hence, it is respectfully submitted that it is clear to one skilled in the art how the method of the present invention is utilized and the physical objects or structures that are analyzed.

With respect to the Examiner's argument that the sets of three-dimensional coordinates are not limited to originate from two different structures, it is respectfully submitted that the selection of coinciding attributes narrows the field of structures so that it is clear to one skilled in the art how to interpret the results of the correspondence comparison.

With respect to the Examiner's argument that the specification does not disclose a utility for comparing different parts of the same compound or molecule, it is respectfully submitted that it is known to those skilled in the art that molecules may be split with enzymes, for example, papain or pepsin, to provided smaller portions of the molecules for further analysis, allowing smaller portions of the molecules to be analyzed and then compared with the known molecules. Such further treatment of the molecules prior to utilizing the method of the present invention is not discussed in the specification because it is known to those skilled in the art. Hence, immediately useful results are readily obtained.

With respect to the Examiner's argument that similarity and utility is not discussed in the specification, it is respectfully submitted that on page 2, lines 22-29, the specification states: "For instance, a commonly existing sequence pattern (region) is known to be found when the amino acid sequences in **proteins having the same function** are compared between different types of organisms. This region is called a motif. Accordingly, if it is possible to extract the motif automatically, the property and function of the protein can be shown by finding which motif is included in the sequence" (emphasis added). Hence, it is respectfully submitted that if the unknown protein and the known protein have a same function, the corresponding motif may be determined by the method of the present invention.

As noted above, when a protein being assayed has a known function, its utility is known, and the method of the present invention may be implemented without requiring further research for utility.

Further, the present invention produces a useful result. For example, FIG. 1 illustrates an embodiment of an apparatus that utilizes the method of the present invention, thus enabling automatic determination of the correspondence/similarity determination with respect to desired molecules, which speeds up the process of such a determination in comparison with a manual determination, which takes a greater amount of time and is unwieldy due to the large amount of data handled.

Thus, the present invention uses a machine to transform data, through a series of mathematical calculations, **to produce a useful result**, which is at least momentarily fixed for recording and reporting purposes. Accordingly, Applicant respectfully requests reconsideration and withdrawal of the rejections of claims 13-15 under 35 U.S.C. §101 because the claimed invention is directed to statutory subject matter and the claimed invention has patentable utility.

REJECTION UNDER 35 U.S.C. §112:

In the Office Action, at page 7, numbered paragraph 6, claims 13-15 were rejected under 35 U.S.C. §112, first paragraph. This rejection is traversed and reconsideration is requested.

As noted above, it is respectfully submitted that on page 2, lines 22-29, the specification states: "For instance, a commonly existing sequence pattern (region) is known to be found when the amino acid sequences in **proteins having the same function** are compared between different types of organisms. This region is called a motif. Accordingly, if it is possible to extract the motif automatically, the property and function of the protein can be shown by finding which motif is included in the sequence" (emphasis added). Hence, it is respectfully submitted that if the unknown protein and the known protein have a same function, the corresponding motif may be determined by the method of the present invention.

As noted above, **when a protein being assayed has a known function, its utility is known**, and the method of the present invention may be implemented without requiring further research for utility.

Thus, it is respectfully submitted that claims 13-15 are clear and patentable under 35 U.S.C. §112, first paragraph.

REJECTION UNDER 35 U.S.C. §102:

In the Office Action, at pages 7-8, numbered paragraph 7, claims 13-15 were rejected under 35 U.S.C. §102(b) as anticipated by USPN 4,853,871 or Holak et al. or Flaherty et al. or Mosimann et al. for the reasons of record. This rejection is traversed and reconsideration is requested.

The Examiner appears to be confused about the values determined in claim 13. Claim 13 determines that when the attribute value of the first set of points coincides with the attribute value of the second set of points, the rmsd is determined between the elements corresponding in the combination of correspondence generated. Thus, by examining the rmsd, it may be determined whether the first set of points and the second set of points coincide or are similar. A predetermined threshold rsmd difference is used to determine same. It is respectfully submitted that none of the references USPN 4,853,871, Holak et al., Flaherty et al., or Mosimann et al. recite this process.

Thus, it is respectfully submitted that claims 13-15 are not anticipated under 35 U.S.C. §102(b) by USPN 4,853,871 or Holak et al. or Flaherty et al. or Mosimann et al.

DOUBLE PATENTING:

In the Office Action, at pages 8-9, numbered paragraph 8, claims 13-15 were rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable

over claims 16, 17 of co-pending application 09/909809 or claims 5-11, 24 of co-pending application 09/910054. The rejection is traversed and reconsideration is requested.

It is respectfully submitted that it is premature to raise a double patenting issue since the conflicting claims have not in fact been patented. Thus, the claims in the co-pending applications 09/909809 and 09/910054 are subject to change, and may not necessarily, in their final form, raise the issue of double patenting. Hence, Applicants respectfully suggest it is premature to reject the claims of the present application on the basis of double patenting.

NEW CLAIMS:

New claim 24 recites that the features of the present invention include a method of analyzing, by a computer, three-dimensional structures including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set; generating a combination of correspondence such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the each of the subsets of the second point set from among all candidates for the combination of correspondence; calculating a root mean square distance (rmsd) between the elements corresponding in the combination of correspondence generated, and where the rmsd is less than a predetermined threshold value, determining that the elements of the first point set coincide with or are similar to the subset of the second point set corresponding in the combination of correspondence generated and storing a correspondence/similarity determination on a computer readable recording medium. Nothing in the prior art teaches or suggests such. It is submitted that this new claim distinguishes over the prior art.

New claim 25 recites that the features of claim 24 of the present invention further include that the second point set is divided into the subsets so that the number of elements belonging to each of the subsets is a function of the number of elements belonging to the first point set. Nothing in the prior art teaches or suggests such. It is submitted that this new claim distinguishes over the prior art.

New claim 26 recites that the features of claim 24 of the present invention further include that the second point set is divided into the subsets so that a spatial size of each of the subsets is nearly equal to a spatial size of the first point set. Nothing in the prior art teaches or suggests such. It is submitted that this new claim distinguishes over the prior art.

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited by the Examiner contacting the undersigned attorney for a telephone interview to discuss resolution of such issues.

If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

STAAS & HALSEY LLP

Date: _July 6, 2005_   By: _Darleen J. Hockley_

Darleen J. Stockley
Registration No. 34,257

1201 New York Avenue, N.W.
Suite 700
Washington, D.C. 20005
Telephone: (202) 434-1500
Facsimile: (202) 434-1501